

SEQUENCE LISTING

<110> Japan Science and Technology Agency

<120> APOPTOSIS-INDUCING AGENT AND METHOD FOR INDUCING APOPTOSIS

<130> PH-2082-PCT

<150> JP 2003-116299

<151> 2003-04-21

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 1853

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(1693)

<300>

<301> Liu, J. et al.

<302> Defective interplay of activators with TFIH in xeroderma
pigmentosum

<303> Cell

<304> 104

<305> 3

<306> 353-353

<307> 2001

<308> GenBank/NM_14281

<309> 2001-12-26

<313> 1 TO 1853

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Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly

1

5

10

15

ggg ggg tcc gag ccg gcg gcg gcg gca gtg gtg gca gcg gga gac 157

Gly Gly Ser Glu Pro Ala Ala Ala Ala Val Val Ala Ala Gly Asp

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25

30

aaa tgg aaa cct cca cag ggc aca gac tcc atc aag atg gag aac ggg 205

Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly

35

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cag agc aca gcc gcc aag ctg ggg ctg cct ccc ctg acg ccc gag cag 253

Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln

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cag gag gcc ctt cag aag gcc aag aag tac gcc atg gag cag agc atc 301

Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile

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aag agt gtg ctg gtg aag cag acc atc gcg cac cag cag cag cag ctc 349

Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu

80 85 90 95

acc aac ctg cag atg gcg gct cag cgg cag cgg gcg ctg gcc atc atg 397

Thr Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met

100 105 110

tgc cgc gtc tac gtg ggc tct atc tac tat gag ctg ggg gag gac acc 445

Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr

115 120 125

atc cgc cag gcc ttt gcc ccc ttt ggc ccc atc aag agc atc gac atg 493

Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met

130 135 140

tcc tgg gac tcc gtc acc atg aag cac aag ggc ttt gcc ttc gtg gag 541

Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu

145 150 155

tat gag gtc ccc gaa gct gca cag ctg gcc ttg gag cag atg aac tcg 589

Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser

160 165 170 175

gtg atg ctg ggg ggc agg aac atc aag gtg ggc aga ccc agc aac ata 637

Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile

180 185 190

ggg cag gcc cag ccc atc ata gac cag ttg gct gag gag gca cgg gcc 685

Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala

195 200 205

ttc aac cgc atc tac gtg gcc tct gtg cac cag gac ctc tca gac gat 733
Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp
210 215 220

gac atc aag agc gtg ttt gag gcc ttt ggc aag atc aag tcc tgc aca 781
Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr
225 230 235

ctg gcc cgg gac ccc aca act ggc aag cac aag ggc tac ggc ttc att 829
Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile
240 245 250 255

gag tac gag aag gcc cag tcg tcc caa gat gct gtg tct tcc atg aac 877
Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn
260 265 270

ctc ttt gac ctg ggt ggc cag tac ttg cgg gtg ggc aag gct gtc aca 925
Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr
275 280 285

ccg ccc atg ccc cta ctc aca cca gcc acg cct gga ggc ctc cca cct 973
Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro
290 295 300

gcc gct gct gtg gca gct gca gcc act gcc aag atc aca gct cag 1021
Ala Ala Ala Val Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln
305 310 315

gaa gca gtg gcc gga gca gcg gtg ctg ggt acc ctg ggc aca cct gga 1069
Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly
320 325 330 335

ctg gtg tcc cca gca ctg acc ctg gcc cag ccc ctg ggc act ttg ccc 1117
Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro
340 345 350

cag gct gtc atg gct gcc cag gca cct gga gtc atc aca ggt gtg acc 1165
Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr
355 360 365

cca gcc cgt cct atc ccg gtc acc atc ccc tcg gtg gga gtg gtg 1213
Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val
370 375 380

aac ccc atc ctg gcc agc cct cca acg ctg ggt ctc ctg gag ccc aag 1261
Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys
385 390 395

aag gag aag gaa gaa gag gag ctg ttt ccc gag tca gag cgg cca gag 1309
Lys Glu Lys Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu
400 405 410 415

atg ctg agc gag cag gag cac atg agc atc tcg ggc agt agc gcc cga 1357
Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg
420 425 430

cac atg gtg atg cag aag ctg ctc cgc aag cag gag tct aca gtg atg 1405

His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met

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gtt ctg cgc aac atg gtg gac ccc aag gac atc gat gac ctg gaa 1453

Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu

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ggg gag gtg aca gag gag tgt ggc aag ttc ggg gcc gtg aac cgc gtc 1501

Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val

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atc atc tac caa gag aaa caa ggc gag gag gag gat gca gaa atc att 1549

Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile

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gtc aag atc ttt gtg gag ttt tcc ata gcc tct gag act cat aag gcc 1597

Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala

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atc cag gcc ctc aat ggc cgc tgg ttt gct ggc cgc aag gtg gtg gct 1645

Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala

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gaa gtg tac gac cag gag cgt ttt gat aac agt gac ctc tct gcg tga 1693

Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala

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cagtggccc tctccccgga cttgcacttg ttccttgtt cctctgggtt ttatagtgtat 1753

acagtggtgt cccccggggcc aggccgcgctc tgcccagccc agcctacagt gcggataaag 1813

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<213> Homo sapiens

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Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly Gln

35 40 45

Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln Gln

50 55 60

Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile Lys

65 70 75 80

Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Leu Thr

85 90 95

Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met Cys

100 105 110

Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr Ile

115 120 125

Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met Ser

130 135 140

Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu Tyr
145 150 155 160
Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser Val
165 170 175
Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile Gly
180 185 190
Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala Phe
195 200 205
Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp Asp
210 215 220
Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr Leu
225 230 235 240
Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile Glu
245 250 255
Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn Leu
260 265 270
Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr Pro
275 280 285
Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro Ala
290 295 300
Ala Ala Val Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln Glu
305 310 315 320
Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly Leu
325 330 335
Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro Gln
340 345 350
Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr Pro
355 360 365
Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val Asn

370 375 380
Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys Lys
385 390 395 400
Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu Met
405 410 415
Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg His
420 425 430
Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met Val
435 440 445
Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu Gly
450 455 460
Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val Ile
465 470 475 480
Ile Tyr Gln Glu Lys Gln Gly Glu Glu Asp Ala Glu Ile Ile Val
485 490 495
Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala Ile
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Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala Glu
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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<212> DNA

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<210> 5

<211> 18

<212> DNA

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gcacctggag tcatcaca

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<210> 6

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<212> DNA

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<212> DNA

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tcctggtcgt acacttca

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<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 10

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 11

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 12

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<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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<210> 13

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

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agacagcgga aggaggcaaga gtgg

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<210> 14

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: synthetic DNA

<400> 14

ctgtgcagct tcggggacct cata

24